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 NEWS 8 Apr 22 Federal Research in Progress (FEDRIP) now available
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FILE 'MEDLINE' ENTERED AT 17:39:58 ON 08 AUG 2002

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L2 36 L1 AND REVIEW/DT

=> duplicate remove l2

PROCESSING COMPLETED FOR L2

L3 36 DUPLICATE REMOVE L2 (0 DUPLICATES REMOVED)

=> d 1-10 bib ab

L3 ANSWER 1 OF 36 MEDLINE

AN 2002109222 MEDLINE

DN 21829853 PubMed ID: 11840678

TI NMR structural study of disulfide intermediates of hen lysozyme: toward unraveling the protein **folding problem**.

AU Segawa Shin-ichi; Noda Yasuo; Yokota Atsushi; Tachibana Hidekishsegawa@kwansei.ac.jp

SO TANPAKUSHITSU KAKUSAN KOSO. PROTEIN, NUCLEIC ACID, ENZYME, (2002 Feb) 47 (2) 145-51. Ref: 8

Journal code: 0413762. ISSN: 0039-9450.

CY Japan

DT Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LA Japanese

FS Priority Journals

EM 200203

ED Entered STN: 20020214

Last Updated on STN: 20020401

Entered Medline: 20020326

L3 ANSWER 2 OF 36 MEDLINE

AN 2001678596 MEDLINE

DN 21574594 PubMed ID: 11717420

TI Structural genomics: an approach to the protein **folding problem**.

AU Montelione G T

CS Center for Advanced Biotechnology and Medicine, Department of Molecular Biology and Biochemistry, Rutgers University, Piscataway, NJ 08854-5638, USA.. guy@cabm.rutgers.edu

NC P50-GM62413 (NIGMS)

SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2001 Nov 20) 98 (24) 13488-9. Ref: 17

Journal code: 7505876. ISSN: 0027-8424.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LA English

FS Priority Journals

EM 200201

ED Entered STN: 20011129

Last Updated on STN: 20020125

Entered Medline: 20020108

L3 ANSWER 3 OF 36 MEDLINE
 AN 2002071546 MEDLINE
 DN 21656358 PubMed ID: 11798093
 TI In vitro studies of membrane protein folding.
 AU Booth P J; Templer R H; Meijberg W; Allen S J; Curran A R; Lorch M
 CS Department of Biochemistry, School of Medical Sciences, University Walk,
 Bristol, UK.. paula.booth@bristol.ac.uk
 SO CRITICAL REVIEWS IN BIOCHEMISTRY AND MOLECULAR BIOLOGY, (2001) 36 (6)
 501-603. Ref: 299
 Journal code: 8903774. ISSN: 1040-9238.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, ACADEMIC)
 LA English
 FS Priority Journals
 EM 200206
 ED Entered STN: 20020125
 Last Updated on STN: 20020606
 Entered Medline: 20020605
 AB The study of membrane protein folding is a new and challenging research
 field. Consequently, there are few direct studies on the in vitro folding
 of membrane proteins. This review covers work aimed at understanding
 folding mechanisms and the intermolecular forces that drive the folding of
 integral membrane proteins. We discuss the kinetic and thermodynamic
 studies that have been undertaken. Our review also draws on closely
 related research, mainly from purification studies of functional membrane
 proteins, and gives an overview of some of the successful methods. A brief
 survey is also given of the large body of mutagenesis and fragment work on
 membrane proteins, as this too has relevance to the **folding**
problem. It is noticeable that the choice of solubilizing
 detergents and lipids can determine the success of the method, and indeed
 it appears that particular lipid properties can be used to control the
 rate and efficiency of folding. This has important ramifications for much
 in vitro folding work in that it aids our understanding of how to obtain
 and handle folded, functional protein. With this in mind, we also cover
 some relevant properties of model, lipid-bilayer systems.

L3 ANSWER 4 OF 36 MEDLINE
 AN 2001402919 MEDLINE
 DN 21347076 PubMed ID: 11455545
 TI Generalized-ensemble algorithms for molecular simulations of biopolymers.
 AU Mitsutake A; Sugita Y; Okamoto Y
 CS Department of Theoretical Studies, Institute for Molecular Science,
 Okazaki, Aichi, Japan.
 SO BIOPOLYMERS, (2001) 60 (2) 96-123. Ref: 140
 Journal code: 0372525. ISSN: 0006-3525.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, ACADEMIC)
 LA English
 FS Priority Journals
 EM 200109
 ED Entered STN: 20010924
 Last Updated on STN: 20010924
 Entered Medline: 20010920
 AB In complex systems with many degrees of freedom such as peptides and
 proteins, there exists a huge number of local-minimum-energy states.
 Conventional simulations in the canonical ensemble are of little use,
 because they tend to get trapped in states of these energy local minima. A
 simulation in generalized ensemble performs a random walk in potential
 energy space and can overcome this difficulty. From only one simulation
 run, one can obtain canonical-ensemble averages of physical quantities as
 functions of temperature by the single-histogram and/or multiple-histogram

reweighting techniques. In this article we review uses of the generalized-ensemble algorithms in biomolecular systems. Three well-known methods, namely, multicanonical algorithm, simulated tempering, and replica-exchange method, are described first. Both Monte Carlo and molecular dynamics versions of the algorithms are given. We then present three new generalized-ensemble algorithms that combine the merits of the above methods. The effectiveness of the methods for molecular simulations in the protein **folding problem** is tested with short peptide systems.

Copyright 2001 John Wiley & Sons, Inc. Biopolymers (Pept Sci) 60: 96-123, 2001

L3 ANSWER 5 OF 36 MEDLINE
AN 2000478903 MEDLINE
DN 20484166 PubMed ID: 11027486
TI Is the unfolded state the Rosetta Stone of the protein **folding problem**?
AU Hammarstrom P; Carlsson U
CS IFM-Department of Chemistry, Linkoping University, Linkoping, S-581 83, Sweden.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2000 Sep 24) 276 (2) 393-8. Ref: 40
Journal code: 0372516. ISSN: 0006-291X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 200010
ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001027
AB Solving the protein **folding problem** is one of the most challenging tasks in the post genomic era. Identification of folding-initiation sites is very important in order to understand the protein folding mechanism. Detection of residual structure in unfolded proteins can yield important clues to the initiation sites in protein folding. A substantial number of studied proteins possess residual structure in hydrophobic regions clustered together in the protein core. These stable structures can work as seeds in the folding process. In addition, local preferences for secondary structure in the form of turns for beta-sheet initiation and helical turns for alpha-helix formation can guide the folding reaction. In this respect the unfolded states, studied at increasing structural resolution, can be the Rosetta Stone of the **protein folding problem**.
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L3 ANSWER 6 OF 36 MEDLINE
AN 2001041022 MEDLINE
DN 20400935 PubMed ID: 10940248
TI Protein folding intermediates and pathways studied by hydrogen exchange.
AU Englander S W
CS Johnson Research Foundation, Philadelphia, Pennsylvania, USA..
walter@HX2.Med.upenn.Edu
SO ANNUAL REVIEW OF BIOPHYSICS AND BIOMOLECULAR STRUCTURE, (2000) 29 213-38.
Ref: 146
Journal code: 9211097. ISSN: 1056-8700.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 200012

ED Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20001207

AB In order to solve the immensely difficult protein-**folding problem**, it will be necessary to characterize the barriers that slow folding and the intermediate structures that promote it. Although protein-folding intermediates are not accessible to the usual structural studies, hydrogen exchange (HX) methods have been able to detect and characterize intermediates in both kinetic and equilibrium modes--as transient kinetic folding intermediates on a subsecond time scale, as labile equilibrium molten globule intermediates under destabilizing conditions, and as infinitesimally populated intermediates in the high free-energy folding landscape under native conditions. Available results consistently indicate that protein-folding landscapes are dominated by a small number of discrete, metastable, native-like partially unfolded forms (PUFs). The PUFs appear to be produced, one from another, by the unfolding and refolding of the protein's intrinsically cooperative secondary structural elements, which can spontaneously create stepwise unfolding and refolding pathways. Kinetic experiments identify three kinds of barrier processes: (a) an initial intrinsic search-nucleation-collapse process that prepares the chain for intermediate formation by pinning it into a condensed coarsely native-like topology; (b) smaller search-dependent barriers that put the secondary structural units into place; and (c) optional error-dependent misfold-reorganization barriers that can cause slow folding, intermediate accumulation, and folding heterogeneity. These conclusions provide a coherent explanation for the grossly disparate folding behavior of different globular proteins in terms of distinct folding pathways.

L3 ANSWER 7 OF 36 MEDLINE
 AN 1999290833 MEDLINE
 DN 99290833 PubMed ID: 10361090
 TI Exposing the kinetic traps in RNA folding.
 AU Treiber D K; Williamson J R
 CS Department of Molecular Biology, Skaggs Institute for Chemical Biology, The Scripps Research Institute, La Jolla, CA 92037, USA..
 treiber@scripps.edu
 SO CURRENT OPINION IN STRUCTURAL BIOLOGY, (1999 Jun) 9 (3) 339-45. Ref: 47
 Journal code: 9107784. ISSN: 0959-440X.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LA English
 FS Priority Journals
 EM 199907
 ED Entered STN: 19990727
 Last Updated on STN: 19990727
 Entered Medline: 19990712

AB Large ribozymes fold on a 'glacial' timescale compared to the folding of their protein counterparts. The sluggish folding exhibited by large RNAs results from the formation of kinetically trapped, misfolded intermediates, which are nonessential features of the folding mechanism. Newly developed mutant ribozymes that avoid kinetic traps should facilitate the study of the RNA **folding problem**.

L3 ANSWER 8 OF 36 MEDLINE
 AN 1999337584 MEDLINE
 DN 99337584 PubMed ID: 10407402
 TI Beyond proteins.
 AU Robson B
 CS Computational Biology Center, IBM T. J. Watson Research Center, 30 Saw Mill River Road, Hawthorne, NY 10523, USA.. robsonb@us.ibm.com
 SO TRENDS IN BIOTECHNOLOGY, (1999 Aug) 17 (8) 311-5. Ref: 22
 Journal code: 8310903. ISSN: 0167-7799.

CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)

LA English
FS Priority Journals
EM 199909
ED Entered STN: 19991012
Last Updated on STN: 19991012
Entered Medline: 19990928

AB Increased understanding of the biological principles of protein structure and folding, combined with advances in protein-synthetic chemistry, should not only allow us to borrow from biology but also to depart from it and so produce protein-like, but non-protein, molecules and molecular devices. However, radical departures from protein-like forms into more-robust and truly novel 'smart' polymers and materials first require a solution to the **protein-folding problem** using only fundamental physicochemical principles. Any such practical solution may not come from raw computing power alone but rather from a deeper understanding of topological principles.

L3 ANSWER 9 OF 36 MEDLINE
AN 2000020729 MEDLINE
DN 20020729 PubMed ID: 10550208
TI How RNA folds.

AU Tinoco I Jr; Bustamante C
CS Department of Chemistry, University of California Berkeley, Berkeley, CA 94720-1460, USA.

NC GM 10840 (NIGMS)
GM 32543 (NIGMS)

SO JOURNAL OF MOLECULAR BIOLOGY, (1999 Oct 22) 293 (2) 271-81. Ref: 55
Journal code: 2985088R. ISSN: 0022-2836.

CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)

LA English
FS Priority Journals
EM 199911
ED Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991119

AB We describe the RNA **folding problem** and contrast it with the much more difficult protein **folding problem**. RNA has four similar monomer units, whereas proteins have 20 very different residues. The folding of RNA is hierarchical in that secondary structure is much more stable than tertiary folding. In RNA the two levels of folding (secondary and tertiary) can be experimentally separated by the presence or absence of Mg²⁺. Secondary structure can be predicted successfully from experimental thermodynamic data on secondary structure elements: helices, loops, and bulges. Tertiary interactions can then be added without much distortion of the secondary structure. These observations suggest a folding algorithm to predict the structure of an RNA from its sequence. However, to solve the RNA **folding problem** one needs thermodynamic data on tertiary structure interactions, and identification and characterization of metal-ion binding sites. These data, together with force versus extension measurements on single RNA molecules, should provide the information necessary to test and refine the proposed algorithm.
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L3 ANSWER 10 OF 36 MEDLINE
AN 1999257331 MEDLINE
DN 99257331 PubMed ID: 10322208
TI New Monte Carlo algorithms for protein folding.

AU Hansmann U H; Okamoto Y
 CS Department of Physics Michigan Technological University, Houghton, MI
 49931-1295, USA.. hansmann@mtu.edu
 SO CURRENT OPINION IN STRUCTURAL BIOLOGY, (1999 Apr) 9 (2) 177-83. Ref: 84
 Journal code: 9107784. ISSN: 0959-440X.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LA English
 FS Priority Journals
 EM 199908
 ED Entered STN: 19990910
 Last Updated on STN: 19990910
 Entered Medline: 19990820
 AB Over the past three decades, a number of powerful simulation algorithms
 have been introduced to the protein **folding problem**.
 For many years, the emphasis has been placed on how to both overcome the
 multiple minima problem and find the conformation with the global minimum
 potential energy. Since the new view of the protein folding mechanism
 (based on the free energy landscape of the protein system) arose in the
 past few years, however, it is now of interest to obtain a global
 knowledge of the phase space, including the intermediate and denatured
 states of proteins. Monte Carlo methods have proved especially valuable
 for these purposes. As well as new, powerful optimization techniques,
 novel algorithms that can sample much a wider phase space than
 conventional methods have been established.

=> d 11-20 bib ab

L3 ANSWER 11 OF 36 MEDLINE
 AN 1998195429 MEDLINE
 DN 98195429 PubMed ID: 9526123
 TI Denatured states of yeast phosphoglycerate kinase.
 AU Damaschun G; Damaschun H; Gast K; Zirwer D
 CS Institut fur Biologie der Humboldt-Universitat zu Berlin, Germany..
 gdamasc@mdc-berlin.de
 SO BIOCHEMISTRY, (1998 Mar) 63 (3) 259-75. Ref: 98
 Journal code: 0376536. ISSN: 0006-2979.
 CY RUSSIA: Russian Federation
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LA English
 FS Priority Journals
 EM 199808
 ED Entered STN: 19980820
 Last Updated on STN: 19980820
 Entered Medline: 19980811
 AB Structures of proteins in unfolded states have important implications for
 the protein **folding problem** and for the translocation
 of polypeptide chains. Acid-denatured, cold-denatured, and 6 M guanidine
 hydrochloride (GuHCl) denatured yeast phosphoglycerate kinase (PGK) are
 ensembles of flexible unfolded molecules with rapidly interconverting
 structures of the individual polypeptide chains. They differ, however, in
 their physical properties, such as in coil size and in stiffness over a
 short distance along the chain. These properties of polypeptide chains can
 be described well by persistence statistics. A solution containing 0.7 M
 GuHCl at 4.5 degrees C is nearly a Theta-solvent for PGK. By contrast, 6 M
 GuHCl is a good solvent for PGK. Acid-denatured PGK at low ionic strength
 has the most expanded and stiffest chains. The conformation of
 heat-denatured PGK should be more compact than that of random walk chains
 at the Theta-point, as can be inferred from measurements on other
 proteins. Investigations of heat-denatured PGK by scattering methods are

unfeasible due to aggregation of the protein. The persistence length as a measure of chain stiffness varies between $a = 1.74$ nm for cold-denatured PGK and $a = 3.0$ nm for acid-denatured PGK. The distribution functions of the gyration radii were calculated from the X-ray scattering data for all unfolded states and compared with the radius of gyration of the natively folded molecule.

L3 ANSWER 12 OF 36 MEDLINE
AN 1999106815 MEDLINE
DN 99106815 PubMed ID: 9890141
TI Protein structure prediction and design.
AU Morea V; Leplae R; Tramontano A
CS IRBM P. Angeletti, Pomezia, Rome, Italy.
SO BIOTECHNOLOGY ANNUAL REVIEW, (1998) 4 177-214. Ref: 160
Journal code: 9616443.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 199902
ED Entered STN: 19990216
Last Updated on STN: 19990216
Entered Medline: 19990202
AB Proteins have a unique native conformation, which can be proven in many instances to be determined by the amino acid sequence alone. The **folding problem**, that is the understanding of how the amino acid sequence directs folding, is still unsolved, despite more than 30 years of effort. However, many new methods have appeared in the past few years. This chapter describes the different principles underlying them and tries to give an overview of their successes and pitfalls.

L3 ANSWER 13 OF 36 MEDLINE
AN 1998179825 MEDLINE
DN 98179825 PubMed ID: 9519299
TI Simplified proteins: minimalist solutions to the 'protein **folding problem**'.
AU Plaxco K W; Riddle D S; Grantcharova V; Baker D
CS Department of Biochemistry, University of Washington, Seattle 98195, USA..
kwp@elina.bchem.washington.edu
SO CURRENT OPINION IN STRUCTURAL BIOLOGY, (1998 Feb) 8 (1) 80-5. Ref: 48
Journal code: 9107784. ISSN: 0959-440X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199805
ED Entered STN: 19980514
Last Updated on STN: 19980514
Entered Medline: 19980501
AB Recent research has suggested that stable, native proteins may be encoded by simple sequences of fewer than the full set of 20 proteogenic amino acids. Studies of the ability of simple amino acid sequences to encode stable, topologically complex, native conformations and to fold to these conformations in a biologically relevant time frame have provided insights into the sequence determinants of protein structure and folding kinetics. They may also have important implications for protein design and for theories of the origins of protein synthesis itself.

L3 ANSWER 14 OF 36 MEDLINE
AN 1998179824 MEDLINE
DN 98179824 PubMed ID: 9519298

TI Pathways for protein folding: is a new view needed?.
 AU Pande V S; Grosberg AY; Tanaka T; Rokhsar D S
 CS Department of Physics, University of California at Berkeley, CA
 94720-7300, USA.. vijay@physics.berkeley.edu
 SO CURRENT OPINION IN STRUCTURAL BIOLOGY, (1998 Feb) 8 (1) 68-79. Ref: 114
 Journal code: 9107784. ISSN: 0959-440X.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LA English
 FS Priority Journals
 EM 199805
 ED Entered STN: 19980514
 Last Updated on STN: 19980514
 Entered Medline: 19980501
 AB Theoretical studies using simplified models of proteins have shed light on
 the general heteropolymeric aspects of the **folding**
problem. Recent work has emphasized the statistical aspects of
 folding pathways. In particular, progress has been made in characterizing
 the ensemble of transition state conformations and elucidating the role of
 intermediates. These advances suggest a reconciliation between the new
 ensemble approaches and the classical view of a folding pathway.

L3 ANSWER 15 OF 36 MEDLINE
 AN 1998357356 MEDLINE
 DN 98357356 PubMed ID: 9692327
 TI Protein design: on the threshold of functional properties.
 AU Tuchscherer G; Scheibler L; Dumy P; Mutter M
 CS Institute of Organic Chemistry, University of Lausanne, Switzerland.
 SO BIOPOLYMERS, (1998) 47 (1) 63-73. Ref: 58
 Journal code: 0372525. ISSN: 0006-3525.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LA English
 FS Priority Journals
 EM 199809
 ED Entered STN: 19980917
 Last Updated on STN: 19990129
 Entered Medline: 19980908
 AB The ultimate goal in protein de novo design is the creation of novel
 macromolecules with tailor-made receptor, sensory, and catalytic
 functions. Despite considerable progress in understanding basic rules of
 secondary structure formation and protein stability, the well-known
 protein **folding problem** is still far from being solved
 and, in general, only a limited number of designed proteins are folded
 uniquely. In this article the state-of-the-art in protein design is
 demonstrated on some selected examples, indicating that the construction
 of protein-like macromolecules mimicking some essential features of
 natural proteins seems to be within reach. Thus, protein design and
 mimicry has become an interdisciplinary challenge with most intriguing
 perspectives.

L3 ANSWER 16 OF 36 MEDLINE
 AN 97348223 MEDLINE
 DN 97348223 PubMed ID: 9204274
 TI Protein-facilitated RNA folding.
 AU Weeks K M
 CS Department of Chemistry, University of North Carolina, Chapel Hill
 27599-3290, USA.. weeks@unc.edu
 SO CURRENT OPINION IN STRUCTURAL BIOLOGY, (1997 Jun) 7 (3) 336-42. Ref: 58
 Journal code: 9107784. ISSN: 0959-440X.
 CY ENGLAND: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)

LA English
 FS Priority Journals
 EM 199708
 ED Entered STN: 19970825
 Last Updated on STN: 19970825
 Entered Medline: 19970808

AB In the absence of protein collaborators, both simple and complex RNAs often misfold or are unfolded. Biologically important RNAs solve their **folding problem**, in part, using the assistance of chaperone and cofactor proteins. Recent work emphasizes several rules for RNA-protein complexes: formation involves induced fit; many large RNAs fold slowly; and ribonucleoprotein assembly requires multiple steps. Finally, protein binding can introduce thermodynamic side effects.

L3 ANSWER 17 OF 36 MEDLINE
 AN 97398939 MEDLINE
 DN 97398939 PubMed ID: 9255068
 TI RNA seeing double: close-packing of helices in RNA tertiary structure.
 AU Strobel S A; Doudna J A
 CS Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, CT 06520, USA.
 NC GM22778-21 (NIGMS)
 GM54839-01 (NIGMS)
 SO TRENDS IN BIOCHEMICAL SCIENCES, (1997 Jul) 22 (7) 262-6. Ref: 49
 Journal code: 7610674. ISSN: 0968-0004.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)

LA English
 FS Priority Journals
 EM 199709
 ED Entered STN: 19970922
 Last Updated on STN: 20000303
 Entered Medline: 19970905

AB Structured RNA molecules play essential roles in RNA processing, chromosome maintenance and protein biosynthesis. RNA necessarily uses different strategies than proteins for folding and assembly of complex architectures. The **RNA-folding problem** is largely an issue of helical packing: how does RNA organize and pack short, double-helical segments to produce active sites and recognition motifs for proteins? Noncanonical base pairs, metal ions and 2'-hydroxyl groups are key elements in RNA higher-order structure formation.

L3 ANSWER 18 OF 36 MEDLINE
 AN 97414929 MEDLINE
 DN 97414929 PubMed ID: 9269572
 TI The Levinthal paradox: yesterday and today.
 AU Karplus M
 CS Laboratoire de Chimie Biophysique, Institute le Bel, Universite Louis Pasteur, Strasbourg, France.. marci@brel.u-strasbg.fr
 SO FOLDING AND DESIGN, (1997) 2 (4) S69-75. Ref: 75
 Journal code: 9604387. ISSN: 1359-0278.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)

LA English
 FS Priority Journals
 EM 199710
 ED Entered STN: 19971013
 Last Updated on STN: 19971013

Entered Medline: 19971001

AB A change in the perception of the protein **folding problem** has taken place recently. The nature of the change is outlined and the reasons for it are presented. An essential element is the recognition that a bias toward the native state over much of the effective energy surface may govern the folding process. This has replaced the random search paradigm of Levinthal and suggests that there are many ways of reaching the native state in a reasonable time so that a specific pathway does not have to be postulated. The change in perception is due primarily to the application of statistical mechanical models and lattice simulations to protein folding. Examples of lattice model results on protein folding are presented. It is pointed out that the new optimism about the protein **folding problem** must be complemented by more detailed studies to determine the structural and energetic factors that introduce the biases which make possible the folding of real proteins.

L3 ANSWER 19 OF 36 MEDLINE

AN 97184701 MEDLINE

DN 97184701 PubMed ID: 9032055

TI The prion **folding problem**.

AU Harrison P M; Bamborough P; Daggett V; Prusiner S B; Cohen F E

CS University of California, Box Number 450, San Francisco, CA-94143, USA.

SO CURRENT OPINION IN STRUCTURAL BIOLOGY, (1997 Feb) 7 (1) 53-9. Ref: 51
Journal code: 9107784. ISSN: 0959-440X.

CY ENGLAND: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LA English

FS Priority Journals

EM 199703

ED Entered STN: 19970327

Last Updated on STN: 19970327

Entered Medline: 19970319

AB Prion diseases are neurodegenerative disorders in which dramatic conformational change in the structure of the prion protein is the fundamental event. This structural transition involves the loss of substantial alpha-helical content and the acquisition of beta-sheet structure. A convergence of recent biological and structural studies argues that the mechanism underlying the prion diseases is truly unprecedented.

L3 ANSWER 20 OF 36 MEDLINE

AN 97181651 MEDLINE

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TI Gramicidin channels--a solvable membrane "protein" **folding problem**.

AU Andersen O S; Saberwal G; Greathouse D V; Koeppe R E 2nd

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AB The linear gramicidins are peptide antibiotics that form cation-selective channels in lipid bilayers. Gramicidin channels have very well-defined functional characteristics, and the structure of membrane-spanning gramicidin A channels is known at atomic resolution. These features make the gramicidins well suited to study how the amino acid sequence encodes the structure and function of a membrane-spanning channel. We show how one can use electrophysiological measurements to obtain structural information about conducting channels and to quantify the conformational preferences of sequence-substituted gramicidin mutants.

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---Logging off of STN---

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Executing the logoff script...

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SESSION

FULL ESTIMATED COST

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10.40

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